Package: asar (via r-universe)

March 10, 2025

Title Build NOAA Stock Assessment Report

Version 1.0.0

Description Build a full or update stock assessment report for any stock assessment model. Parameterization allows the user to call a template based on their regional science center, species, area, ect.

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URL https://github.com/nmfs-ost/asar

Depends R (>= 2.10)

Imports dplyr, flextable, forstringr, fs, ggplot2, glue, gridExtra, naniar, nmfspalette, officer, openxlsx, prodlim, quarto, stats, stringr, svDialogs, tibble, tidyr, tidyselect, tinytex, utils, withr

Suggests gt, kableExtra, knitr, parallel, r4ss, rmarkdown, snowfall, stockplotr, testthat (>= 3.0.0)

VignetteBuilder knitr

Remotes nmfs-fish-tools/nmfspalette, nmfs-ost/stockplotr, r4ss/r4ss

Config/testthat/edition 3

Config/testthat/parallel false

Encoding UTF-8

Language en-US

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Config/pak/sysreqs libcairo2-dev libfontconfig1-dev libfreetype6-dev libfribidi-dev make libharfbuzz-dev libicu-dev libjpeg-dev libpng-dev libtiff-dev libxml2-dev libssl-dev libx11-dev

Repository https://nmfs-ost.r-universe.dev

RemoteUrl https://github.com/nmfs-ost/asar

RemoteRef HEAD

RemoteSha 6170630520bffdcfecfe863ddc24447d08ecd2f4

Contents

`add_alttext` *Add alternative text into latex*

Description

Add alternative text into latex

Usage

```
add_alttext(
  x = list.files(getwd())[grep("skeleton.tex", list.files(getwd()))],
  dir = getwd(),
  rda_dir = getwd(),
  alttext_csv_dir = getwd(),
  compile = TRUE,
  rename = NULL
)
```

Arguments

`x`	.tex file containing report. Typically produced after initially rendering the skeleton made from create_template.
`dir`	directory where the tex file is located that will be edited
`rda_dir`	folder where rda files containing alternative text is located
`alttext_csv_dir`	Directory for the csv file containing alternative text and captions generated when running stockplotr::exp_all_figs_tables

`compile`	Indicate whether the document (X) should be rendered after these files are changed. Default TRUE.
`rename`	Indicate a name for the new tex file produced from this function. There is no need to include ".tex" in the name. Defaults to current name and overwrites the current tex file.

Value

This function was made to help add in alternative text to latex documents generated from quarto. Quarto does not currently contain a way to add alternative text to PDF documents, so this function was developed as a work around. The addition of alternative text needs to be found in either the rda files produced from stockplotr::exp_all_figs_tables or in the captions_alt_text.csv also produced from the same function. Users not using this format should create a csv file with columns containing "label" and "alt_text".

Examples

```
## Not run:
create_template(
  new_template = TRUE,
  format = "pdf",
  office = "NWFSC",
  region = "U.S. West Coast",
  species = "Dover sole",
  spp_latin = "Microstomus pacificus",
  year = 2010,
  author = c("John Snow", "Danny Phantom", "Patrick Star"),
  include_affiliation = TRUE,
  convert_output = TRUE,
  resdir = "C:/Users/Documents/Example_Files",
  model_results = "Report.sso",
  model = "SS3",
  new_section = "an_additional_section",
  section_location = "after-introduction",
  rda_dir = getwd()
)

path <- getwd()

quarto::quarto_render(file.path(path, "report", "SAR_USWC_Dover_sole_skeleton.qmd"))

withr::with_dir(
  file.path(path, "report"),
  add_alttext(
    x = "SAR_USWC_Dover_sole_skeleton.tex",
    dir = getwd(),
    alttext_csv_dir = getwd(),
    rda_dir = path,
    compile = TRUE,
    rename = "SAR_Dover_sole_tagged"
  )
)
```

```
## End(Not run)
```

`add_base_section` *Add selected sections to outline*

Description

Add selected sections to outline

Usage

```
add_base_section(custom_sections)
```

Arguments

`custom_sections`	List of existing sections to include in the custom template. Note: this only includes sections within list.files(system.file("templates", "skeleton", package = "asar")). The name of the section, rather than the name of the file, can be used (e.g., 'abstract' rather than '00_abstract.qmd'). If adding a new section, also use parameters 'new_section' and 'section_location'.

Value

Call and copy the sections in the package templates to create an outline for a stock assessment

Examples

```
add_base_section(c("executive summary", "assessment", "results"))
```

`add_child` *Write R Chunk to Add Child Document*

Description

Write R Chunk to Add Child Document

Usage

```
add_child(x, label = NULL)
```

Arguments

`x`	An additional section to add into the template. Options for additional sections are in the 'skeleton' folder. Appropriate files are .qmd files and are formatted as such: XX_section.qmd (i.e., not a, b, c... subfiles).
`label`	Description of the child document being added. It should be short- one or two words, maximum.

Value

Formatting R chunk for child document to add section into the template/skeleton. Utilize the cat() function to implement into readable text.

Examples

```
add_child("test_quarto.qmd", label = "test_doc")
```

`add_chunk` *Write R chunk to template*

Description

Write R chunk to template

Usage

```
add_chunk(
  x,
  echo = "false",
  warnings = "false",
  eval = "true",
  label = NULL,
  add_option = FALSE,
  chunk_op = NULL,
  rmark_op = NULL
)
```

Arguments

`x`	Content to be written within the R chunk. Wrap in quotation marks ("").
`echo`	TRUE/FALSE; Option to repeat code in the document. Default is false.
`warnings`	TRUE/FALSE; Option to report warnings in the console during render. Default is false.
`eval`	TRUE/FALSE; Option to evaluate the chunk. Default is true.
`label`	The name of the chunk in the 'label:' section of the R code chunk. This should be in snakecase (i.e., in which words are written in lowercase and connected by underscores).

`add_option`	TRUE/FALSE; Option to add additional chunk options. Default is false.
`chunk_op`	List of chunk options to add. For example: c("output: true", "error: false)
`rmark_op`	List of chunk options to add after indicating the language of the chunk as used in Rmarkdown.

Value

Write an additional R chunk into the template using this function. The code can be written as usual, just remember to put it entirely in quotes for the function to render it properly

Examples

```
add_chunk("plot(cars$speed, cars$distance)")
```

`add_section` *Add New Section or Subsection to Template*

Description

Add New Section or Subsection to Template

Usage

```
add_section(
  new_section = NULL,
  section_location = NULL,
  custom_sections = NULL,
  custom = TRUE,
  subdir = NULL
)
```

Arguments

`new_section`	Names of section(s) (e.g., introduction, results) or subsection(s) (e.g., a section within the introduction) that will be added to the document. Please make a short list if >1 section/subsection will be added. The template will be created as a quarto document, added into the skeleton, and saved for reference.
`section_location`	Where new section(s)/subsection(s) will be added to the skeleton template. Please use the notation of ’placement-section’. For example, ’in-introduction’ signifies that the new content would be created as a child document and added into the 02_introduction.qmd. To add >1 (sub)section, make the location a list corresponding to the order of (sub)section names listed in the ’new_section’ parameter.

`custom_sections`	List of existing sections to include in the custom template. Note: this only includes sections within list.files(system.file("templates", "skeleton", package = "asar")). The name of the section, rather than the name of the file, can be used (e.g., 'abstract' rather than '00_abstract.qmd'). If adding a new section, also use parameters 'new_section' and 'section_location'.
`custom`	TRUE/FALSE; Build custom sectioning for the template, rather than the default for stock assessments in your region? Default is false.
`subdir`	Directory where the new sections will be saved. In the create_template function, this defaults to the location where the template is saved.

Value

Add an additional section or subsection to the report template if it is not already present in the default template. This provides the option to add it as a section before or after an existing section, or within a section as a child document. For developers: this function creates a list of sections that will be added to the skeleton file made from create_template.

Examples

```
add_section(
  new_section = "Ecosystem Considerations", section_location = "after-discussion",
  custom_sections = c("introduction.qmd", "model.qmd", "results.qmd", "discussion.qmd"),
  subdir = tempdir()
)
```

`convert_output` *Convert Output*

Description

Format stock assessment output files to a standardized format.

Usage

```
convert_output(
  output_file = NULL,
  outdir = getwd(),
  model = NULL,
  fleet_names = NULL,
  file_save = FALSE,
  savedir = getwd(),
  save_name = "std_model_output"
)
```

Arguments

`output_file`	Assessment model output file (e.g., the Report.sso file for SS3, the rdat file for BAM, etc.)
`outdir`	Directory of the assessment model output file. Defaults to working directory.
`model`	Assessment model used in evaluation ("ss3", "bam", "asap", "fims", "amak", "ms-java", "wham", "mas").
`fleet_names`	Names of fleets in the assessment model as shortened in the output file. If fleet names are not properly read, then indicate the fleets names as an acronym in a vector
`file_save`	TRUE/FALSE; Save the formatted object rather than calling the function and adding the formatted object to the global environment? Default is false.
`savedir`	Directory to save the converted output file. Defaults to working directory.
`save_name`	Name of the converted output file (do not use spaces).

Value

A reformatted and standardized version of assessment model results for application in building a stock assessment reports and to easily adapt results among regional assessments. The resulting object is simply a transformed and machine readable version of a model output file. There are 2 options for adding data to the function. (1) Add the full path with the file name in output.file or (2) output.file is the file name and outdir is the path to the file without a trailing forward slash.

Author(s)

Samantha Schiano

`create_citation` *Generate Citation for Stock Assessment Report*

Description

Generate Citation for Stock Assessment Report

Usage

```
create_citation(author = NULL, title = NULL, year = NULL, office = NULL)
```

Arguments

`author`	Ordered list of authors included in the assessment.
`title`	The alternative title. Example: "Management Track Assessments Spring 2024".
`year`	Year the assessment is being conducted. Default is the year in which the report is rendered.
`office`	Regional Fisheries Science Center producing the report (i.e., AFSC, NEFSC, NWFSC, PIFSC, SEFSC, SWFSC).

Value

Generate a citation for use in publications and other references associated with the stock assessment report produced with `asar`.

Examples

```
create_citation(
  title = "SA Report for Jellyfish",
  author = c("John Snow", "Danny Phantom", "Patrick Star"),
  year = 2024, office = "NEFSC"
)
```

`create_figures_doc` *Create Quarto Document of Figures*

Description

Create Quarto Document of Figures

Usage

```
create_figures_doc(subdir = NULL, include_all = TRUE, rda_dir = NULL)
```

Arguments

`subdir`	Location of subdirectory storing the assessment report template
`include_all`	TRUE/FALSE; Option to include all default figures for a stock assessment report. Default is true.
`rda_dir`	If the user has already created .rda files containing figures, tables, alt text, and captions with `stockplotr`, rda_dir represents the location of the folder containing these .rda files ("rda_files"). Otherwise, if the user has not used `stockplotr` to make those .rda files already, those files will be generated automatically and placed within an "rda_files" folder within rda_dir. The "rda_files" folder would have been made with `stockplotr::exp_all_figs_tables()`, or by exporting files by running individual `stockplotr` figure- and table-generating functions. If you have used `stockplotr` to generate these .rda files, you can leave the arguments below blank. NOTE: If an "rda_files" folder is detected within rda_dir, .rda files will not be regenerated.

Value

A quarto document with pre-loaded R chunk that adds the stock assessment tables from the nmfs-ost/stockplotr R package. The quarto document will become part of the stock assessment outline.

`create_inheader_tex` *Create in-header latex document*

Description

Create in-header latex document

Usage

```
create_inheader_tex(species = NULL, year = NULL, subdir)
```

Arguments

`species`	common species name - used for footer
`year`	year assessment is conducted
`subdir`	directory where other files will be copied into

Value

Create an in-header latex document that dynamically changes based on the species and year along with other factors.

`create_tables_doc` *Create Quarto Document of Tables*

Description

Create Quarto Document of Tables

Usage

```
create_tables_doc(subdir = NULL, include_all = TRUE, rda_dir = NULL)
```

Arguments

`subdir`	subdirectory where the assessment report template is being stored
`include_all`	include all default tables for a stock assessment report
`rda_dir`	If the user has already created .rda files containing figures, tables, alt text, and captions with `stockplotr`, rda_dir represents the location of the folder containing these .rda files ("rda_files"). Otherwise, if the user has not used `stockplotr` to make those .rda files already, those files will be generated automatically and placed within an "rda_files" folder within rda_dir. The "rda_files" folder would have been made with `stockplotr::exp_all_figs_tables()`, or by exporting files by running individual `stockplotr` figure- and table-generating functions. If you have used `stockplotr` to generate these .rda files, you can leave the arguments below blank. NOTE: If an "rda_files" folder is detected within rda_dir, .rda files will not be regenerated.

Value

Create a quarto document as part of a stock assessment outline with pre-loaded R chunk adding the stock assessment tables from the nmfs-ost/stockplotr R package. NOTE: If your table is too wide to print on a portrait-oriented page, the page will be rotated to landscape view. If if is too wide to print in landscape view, it will be split into multiple tables. In this case, a new rda will be created and is identifiable by the phrase "split" in the filename (e.g., indices.abundance_table.rda will generate a new indices.abundance_table_split.rda file). These tables will share the same caption.

`create_template` *Create Stock Assessment Report Template*

Description

To see templates included in the base skeleton, please run 'list.files(system.file('templates','skeleton', package = 'asar'))' in the console.

Usage

```
create_template(
  new_template = TRUE,
  format = c("pdf", "docx", "html", NULL),
  office = c("AFSC", "PIFSC", "NEFSC", "NWFSC", "SEFSC", "SWFSC"),
  region = NULL,
  complex = FALSE,
  species = NULL,
  spp_latin = NULL,
  year = NULL,
  file_dir = getwd(),
  author = "",
  add_author = NULL,
  include_affiliation = TRUE,
  simple_affiliation = FALSE,
  alt_title = FALSE,
  title = NULL,
  parameters = TRUE,
  param_names = NULL,
  param_values = NULL,
  convert_output = FALSE,
  fleet_names = NULL,
  resdir = NULL,
  model_results = NULL,
  model = NULL,
  new_section = NULL,
  section_location = NULL,
  type = "SAR",
  prev_year = NULL,
```

```
  custom = FALSE,
  custom_sections = NULL,
  include_figures = TRUE,
  include_tables = TRUE,
  add_image = FALSE,
  spp_image = NULL,
  bib_file = "asar_references.bib",
  rda_dir = getwd(),
  end_year = NULL,
  n_projected_years = 10,
  relative = FALSE,
  recruitment_scale_amount = 1,
  recruitment_unit_label = "metric tons",
  ref_line = c("target", "MSY", "msy", "unfished"),
  ref_point = NULL,
  biomass_scale_amount = 1,
  landings_unit_label = "metric tons",
  ref_point_sb = NULL,
  spawning_biomass_label = "metric tons",
  spawning_biomass_scale_amount = 1,
  ref_line_sb = c("target", "MSY", "msy", "unfished"),
  indices_unit_label = "",
  biomass_unit_label = "mt",
  catch_unit_label = "mt"
)
```

Arguments

`new_template`	TRUE/FALSE; Create a new template? If true, will pull the last saved stock assessment report skeleton. Default is false.
`format`	Rendering format (pdf, html, or docx).
`office`	Regional Fisheries Science Center producing the report (i.e., AFSC, NEFSC, NWFSC, PIFSC, SEFSC, SWFSC).
`region`	Full name of region in which the species is evaluated (if applicable). If the region is not specified for your center or species, do not use this variable.
`complex`	TRUE/FALSE; Is this a species complex? Default is false.
`species`	Full common name for target species. Split naming with a space and capitalize first letter(s). Example: "Dover sole".
`spp_latin`	Latin name for the target species. Example: "Pomatomus saltatrix".
`year`	Year the assessment is being conducted. Default is the year in which the report is rendered.
`file_dir`	Location of stock assessment files produced by this function. Default is the working directory.
`author`	Ordered list of authors included in the assessment.
`add_author`	Author that is not currently in the database and who should be temporarily added to the author list. Format as "First MI Last". Please leave a comment on the GitHub issues page to be added.

`include_affiliation`	TRUE/FALSE; Does the analyst want to include the authors' affiliations in the document? Default is false.
`simple_affiliation`	TRUE/FALSE; If including affiliations, should the office name function as the affiliation, rather than the full address? Default is true.
`alt_title`	TRUE/FALSE; Use a title that is not the default title (i.e., an alternative title)? Default is false.
`title`	The alternative title. Example: "Management Track Assessments Spring 2024".
`parameters`	TRUE/FALSE; For parameterization of the script. Default is true.
`param_names`	List of parameter names that will be called in the document. Parameters automatically included: office, region, species (each of which are listed as individual parameters for this function, above).
`param_values`	List of values associated with the order of parameter names. Parameters automatically included: office, region, species (each of which are listed as individual parameters for this function, above).
`convert_output`	TRUE/FALSE; Convert the output file to standard model format while creating report template? Default is false.
`fleet_names`	Deprecated: List of fleet names as described in BAM output file (abbreviations).
`resdir`	Filepath of the directory storing the model results file(s). Examples where dover_sole_2024 is the project root for absolute and relative filepaths, respectively: "C:/Users/patrick.star/Documents/dover_sole_2024/models", "here::here("models")".
`model_results`	The model results file. Before the stock assessment output file has been converted to a standardized format with the function convert_output.R, the model results file may be a .sso or .rdata file. After conversion, this file will be a .csv file.
`model`	Type of assessment model that was used to assess the stock (e.g., "BAM", "SS3", "AMAK", "ASAP", etc.).
`new_section`	Names of section(s) (e.g., introduction, results) or subsection(s) (e.g., a section within the introduction) that will be added to the document. Please make a short list if >1 section/subsection will be added. The template will be created as a quarto document, added into the skeleton, and saved for reference.
`section_location`	Where new section(s)/subsection(s) will be added to the skeleton template. Please use the notation of 'placement-section'. For example, 'in-introduction' signifies that the new content would be created as a child document and added into the 02_introduction.qmd. To add >1 (sub)section, make the location a list corresponding to the order of (sub)section names listed in the 'new_section' parameter.
`type`	Type of report to build. Default is SAR.
`prev_year`	Year in which the previous assessment report was conducted. Used to pull previous assessment template.
`custom`	TRUE/FALSE; Build custom sectioning for the template, rather than the default for stock assessments in your region? Default is false.

`custom_sections`	List of existing sections to include in the custom template. Note: this only includes sections within list.files(system.file("templates", "skeleton", package = "asar")). The name of the section, rather than the name of the file, can be used (e.g., ’abstract’ rather than ’00_abstract.qmd’). If adding a new section, also use parameters ’new_section’ and ’section_location’.
`include_figures`	TRUE/FALSE; Should figures be included in the report? Default is true.
`include_tables`	TRUE/FALSE; Should tables be included in the report? Default is true.
`add_image`	TRUE/FALSE; Add image of species to the template that is not already included in the project’s inst/resources/spp_img folder? Default is false.
`spp_image`	File path to the species’ image if not using the image included in the project’s repository.
`bib_file`	File path to a .bib file used for citing references in the report
`rda_dir`	If the user has already created .rda files containing figures, tables, alt text, and captions with `stockplotr`, rda_dir represents the location of the folder containing these .rda files ("rda_files"). Otherwise, if the user has not used `stockplotr` to make those .rda files already, those files will be generated automatically and placed within an "rda_files" folder within rda_dir. The "rda_files" folder would have been made with `stockplotr::exp_all_figs_tables()`, or by exporting files by running individual `stockplotr` figure- and table-generating functions. If you have used `stockplotr` to generate these .rda files, you can leave the arguments below blank. NOTE: If an "rda_files" folder is detected within rda_dir, .rda files will not be regenerated.
`end_year`	The last year of assessment. The default is year - 1.
`n_projected_years`	Number of years spawning biomass is projected for. By default this number is set to 10
`relative`	A logical value specifying if the resulting figures should be relative spawning biomass. The default is ’FALSE’. ’ref_line’ indicates which reference point to use.
`recruitment_scale_amount`	A number describing how much to scale down the recruitment quantities shown on the y axis. For example, recruitment_scale_amount = 100 would scale down a value from 500,000 –> 5,000. This scale will be reflected in the y axis label.
`recruitment_unit_label`	Units for recruitment
`ref_line`	An argument inherited from `stockplotr::plot_spawning_biomass.R`. A string specifying the type of reference you want to compare spawning biomass to. The default is `"target"`, which looks for `"spawning_biomass_target"` in the `"label"` column of `dat`. The actual searching in `dat` is case agnostic and will work with either upper- or lower-case letters but you must use one of the options specified in the default list to ensure that the label on the figure looks correct regardless of how it is specified in `dat`.

`ref_point`	An argument inherited from `stockplotr::plot_biomass.R`. A known value of the reference point along with the label for the reference point as specified in the output file. Please use this option if the ref_line cannot find your desired point. Indicate the reference point in the form c("label" = value).
`biomass_scale_amount`	A number describing how much to scale down the biomass quantities shown on the y axis. See `recruitment_scale_amount`.
`landings_unit_label`	Units for landings
`ref_point_sb`	Identical definition as `ref_point`, but this argument is applied to plot_spawning_biomass.
`spawning_biomass_label`	Units for spawning biomass
`spawning_biomass_scale_amount`	A number describing how much to scale down the spawning biomass quantities shown on the y axis. See `recruitment_scale_amount`.
`ref_line_sb`	A string specifying the type of reference you want to compare spawning biomass to. The default is `"target"`, which looks for `"spawning_biomass_target"` in the `"label"` column of `dat`. The actual searching in `dat` is case agnostic and will work with either upper- or lower-case letters but you must use one of the options specified in the default list to ensure that the label on the figure looks correct regardless of how it is specified in `dat`.
`indices_unit_label`	Units for index of abundance/CPUE
`biomass_unit_label`	Abbreviated units for biomass
`catch_unit_label`	Abbreviated units for catch

Value

Create template and pull skeleton for a stock assessment report. Function builds a YAML specific to the region and utilizes current resources and workflows from different U.S. Fishery Science Centers. General sections are called as child documents in this skeleton and each of the child documents should be edited separately.

Examples

```
## Not run:
create_template(
  new_section = "a_new_section",
  section_location = "before-introduction",
  rda_dir = here::here()
)


create_template(
  new_template = TRUE,
  format = "pdf",
```

```
  office = "NWFSC",
  species = "Dover sole",
  spp_latin = "Microstomus pacificus",
  year = 2010,
  author = c("John Snow", "Danny Phantom", "Patrick Star"),
  include_affiliation = TRUE,
  resdir = "C:/Users/Documents/Example_Files",
  model_results = "Report.sso",
  model = "SS3",
  new_section = "an_additional_section",
  section_location = "after-introduction",
  rda_dir = here::here()
)

asar::create_template(
  new_template = TRUE,
  format = "pdf",
  office = "PIFSC",
  species = "Striped marlin",
  spp_latin = "Kajikia audax",
  year = 2018,
  author = "Alba Tross",
  model = "BAM",
  new_section = c("a_new_section", "another_new_section"),
  section_location = c("before-introduction", "after-introduction"),
  custom = TRUE,
  custom_sections = c("executive_summary", "introduction"),
  rda_dir = here::here()
)

create_template(
  new_template = TRUE,
  format = "pdf",
  office = "NWFSC",
  region = "my_region",
  complex = FALSE,
  species = "Bluefish",
  spp_latin = "Pomatomus saltatrix",
  year = 2010,
  author = c("John Snow", "Danny Phantom", "Patrick Star"),
  add_author = "Sun E Day",
  include_affiliation = TRUE,
  simple_affiliation = TRUE,
  alt_title = FALSE,
  title = "Management Track Assessments Spring 2024",
  parameters = TRUE,
  param_names = c("region", "year"),
  param_values = c("my_region", "2024"),
  convert_output = FALSE,
  fleet_names = c("fleet1", "fleet2", "fleet3"),
  resdir = "C:/Users/Documents/Example_Files",
  model_results = "Report.sso",
  model = "SS3",
```

```
  new_section = "an_additional_section",
  section_location = "before-discussion",
  type = "SAR",
  prev_year = 2021,
  custom = TRUE,
  custom_sections = c("executive_summary", "introduction", "discussion"),
  include_figures = TRUE,
  include_tables = TRUE,
  add_image = TRUE,
  spp_image = "dir/containing/spp_image",
  rda_dir = "C:/Users/Documents",
  end_year = 2022,
  n_projected_years = 10,
  relative = FALSE,
  recruitment_scale_amount = 10,
  recruitment_unit_label = "metric tons",
  ref_line = "target",
  biomass_scale_amount = 100,
  landings_unit_label = "metric tons",
  spawning_biomass_label = "metric tons",
  spawning_biomass_scale_amount = 1000,
  recruitment_unit_label = "metric tons",
  ref_line_sb = "target",
  indices_unit_label = "CPUE",
  biomass_unit_label = "mt",
  catch_unit_label = "mt"
)

## End(Not run)
```

`create_title` *Write Stock Assessment Title*

Description

Write Stock Assessment Title

Usage

```
create_title(
  office = NULL,
  species = NULL,
  region = NULL,
  year = NULL,
  complex = NULL,
  type = NULL,
  spp_latin = NULL
)
```

Arguments

`office`	Regional Fisheries Science Center producing the report (i.e., AFSC, NEFSC, NWFSC, PIFSC, SEFSC, SWFSC).
`species`	Full common name for target species. Split naming with a space and capitalize first letter(s). Example: "Dover sole".
`region`	Full name of region in which the species is evaluated (if applicable). If the region is not specified for your center or species, do not use this variable.
`year`	Year the assessment is being conducted. Default is the year in which the report is rendered.
`complex`	TRUE/FALSE; Is this a species complex? Default is false.
`type`	Type of report to build. Default is SAR.
`spp_latin`	Latin name for the target species. Example: "Pomatomus saltatrix".

Examples

```
create_title(
  office = "SEFSC", species = "Red Snapper", region = "South Atlantic",
  year = 2024, type = "SAR", spp_latin = "Lutjanus campechanus"
)
```

`create_titlepage_tex` *Create a title page latex document*

Description

Create a title page latex document

Usage

```
create_titlepage_tex(office = "", subdir, species)
```

Arguments

`office`	primary science center writing the document
`subdir`	directory where files are going to be held
`species`	target species for assessment

Value

Create a _titlepage.tex document that contains formatting options for a cover page. The only thing that changes currently is the primary author's fishery science center.

`export_object` *Export report object*

Description

Function to export specified object from R environment found in the stock assessment report.

Usage

```
export_object(object = NULL, file_format = "docx", subdir = NULL)
```

Arguments

`object`	Table, plot, or other object in the R environment to export for reference outside of the report document.
`file_format`	The format of the exported file. Options include pdf, docx, xlsx, csv, and rdata. Default is docx.
`subdir`	Directory where object will be exported.

Value

Objects put through this function will be put into the folder "exported" for better organization; DO NOT PUSH THESE TO THE REPO

Author(s)

Samantha Schiano

Examples

```
source <- c("NMFS Groundfish Survey", "", "U.S. Trawl Fisheries", "", "")
data <- c("Survey biomass", "Age Composition", "Catch", "Age Composition", "Length Composition")
years <- c(
  "1984-1999 (triennial), 2001-2013 (biennial)",
  "1984, 1987, 1990, 1993, 1996, 1999, 2003, 2005, 2007, 2009, 2011", "1961-2013",
  "1990,1998-2002, 2004, 2005, 2006, 2008, 2010", "1963-1977, 1991-1997"
)
test_obj <- data.frame(source, data, years)

export_object(object = test_obj, file_format = "csv", subdir = "~")
```

`format_quarto` *Add Formatting Arguments for YAML Header*

Description

Add Formatting Arguments for YAML Header

Usage

```
format_quarto(format = NULL)
```

Arguments

`format`	Rendering format (pdf, html, or docx).

Value

This function returns part of a quarto YAML header involved in formatting the document during rendering.

Examples

```
format_quarto(format = "pdf")
```

`render_lg_table` *Split an extra-wide table into multiple tables*

Description

Split an extra-wide table into multiple tables

Usage

```
render_lg_table(
  report_flextable = NULL,
  essential_columns = NULL,
  rda_dir = NULL,
  plot_name = NULL
)
```

Arguments

`report_flextable`	The extra-wide flextable.
`essential_columns`	The columns that will be retained between the split tables, formatted as a sequence (e.g., 1:2 for columns 1-2, or 1 for a single column. Example: for the indices table, this could be the year column.
`rda_dir`	folder where rda files containing alternative text is located
`plot_name`	name of the .rda file that the table is located from

Value

A list of the split tables.

Examples

```
## Not run:
render_lg_table(
  report_flextable = indices_table,
  essential_columns = 1,
  rda_dir = here::here(),
  plot_name = "indices.abundance_table.rda"
)

render_lg_table(
  report_flextable = important_table,
  essential_columns = 1:3,
  rda_dir = "data",
  plot_name = "bnc_table.rda"
)

## End(Not run)
```

Index